REMARKS

In response to the Restriction Requirement dated August 11, 2009, Applicant has elected Group I, original claims 1-13, directed to an oligonucleotide analog compound, for examination at this time. Applicant further elects the viral family of Flaviviridae, and elects, with traverse, SEQ ID NO:7, targeted to Hepatitis C virus (HCV). Claims 1-7 and 13 read on the elected viral family of Flaviviridae and the elected species of SEQ ID NO:7.

Without acquiescence, and without prejudice to the filing of any divisional, continuation, continuation-in-part, or re-issue application, claims 1, 14, 27, and 29 are amended to focus on the Flaviviridae family, as elected, and claims 8-12 and 22-26 are canceled. No new matter has been added by the amendments.

As to the traversal of the sequence election, Applicants respectfully submit that each of the *flavivirus* antisense targeting sequences in claims 7 and 22 provide a special technical feature over the cited art. As recited in the claims, these targeting sequences are directed to a region associated with stem-loop secondary structure within the 3'-terminal end 40 bases of the negative-sense RNA strand of a *flavivirus*, chosen from St Louis encephalitis virus, Japanese encephalitis virus, Murray Valley encephalitis virus, West Nile fever virus, Yellow fever virus, Dengue type 2 virus, and Hepatitis C virus.

The cited references, alone or in combination, fail to teach or suggest the design of oligonucleotides targeting the 3'-terminal end 40 bases of a *flavivirus*, as claimed. For instance, the International Preliminary Report on Patentability agrees that Stein et al. (WO 2003/033657) fail to teach such oligonucleotides, because this reference targets an entirely different viral region. Neither Anderson et al. (U.S. Patent No. 5,985,662) nor Banerjee et al. (*Virology*. 280:41-51, 2002) remedy the deficiencies in Stein et al., because these references are limited to unrelated viruses, mainly poliovirus (a picornavirus) and hepatitis B virus (HBV), a hepadnavirus), respectively. None of these references even remotely teach or suggest targeting the 3'-terminal end 40 bases of a *flavivirus*, and therefore provide no technical reason to expect such an approach to be successful in reducing flaviviral replication. Because the individual sequences in claims 7 and 22 each target the 3'-terminal end 40 bases of a *flavivirus*, these sequences share a special technical feature that cannot be found in the cited art. Applicant thus

submits that these sequences (SEQ ID NOS:1-7) share Unity of Invention under Article 13.2 PCT.

Accordingly, Applicant respectfully requests reconsideration and withdrawal of the Examiner's requirement to elect a single sequence in these claims, and further requests examination of SEQ ID NOS:1-6 along with SEQ ID NO:7. Consideration of the elected claims is now requested.

Respectfully submitted,

SEED Intellectual Property Law Group PLLC

/Mark E. Rogel/

Mark E. Rogel, J.D.
Registration No. 64,911

MER:rp

701 Fifth Avenue, Suite 5400
Seattle, Washington 98104
Phone: (206) 622-4900
Fax: (206) 682-6031
1502688_1.DOC